

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/722,045

Source: EFW

Date Processed by STIC: 11-19-04

# **ENTERED**



IFWO

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/722,045**

DATE: 11/19/2004  
 TIME: 16:50:33

Input Set : D:\7682108999.txt  
 Output Set: N:\CRF4\11192004\J722045.raw

3 <110> APPLICANT: DeJong, Jan  
 4 Fouchier, Ronaldus  
 5 Van Den Hoogen, Bernadetta  
 6 Osterhaus, Albertus  
 7 Groen, Jan  
 9 <120> TITLE OF INVENTION: Virus causing respiratory tract illness in susceptible mammals

(pg. 6)

11 <130> FILE REFERENCE: 7862-108-999  
 13 <140> CURRENT APPLICATION NUMBER: 10/722,045  
 14 <141> CURRENT FILING DATE: 2003-11-25  
 16 <150> PRIOR APPLICATION NUMBER: 10/466,811  
 17 <151> PRIOR FILING DATE: 2003-07-18  
 19 <150> PRIOR APPLICATION NUMBER: PCT/NL02/00040  
 20 <151> PRIOR FILING DATE: 2002-01-18  
 22 <150> PRIOR APPLICATION NUMBER: EP01200213.5  
 23 <151> PRIOR FILING DATE: 2001-01-19  
 25 <150> PRIOR APPLICATION NUMBER: EP01203985.5  
 26 <151> PRIOR FILING DATE: 2001-10-18  
 28 <160> NUMBER OF SEQ ID NOS: 165  
 30 <170> SOFTWARE: PatentIn version 3.2  
 32 <210> SEQ ID NO: 1  
 33 <211> LENGTH: 394  
 34 <212> TYPE: PRT  
 35 <213> ORGANISM: Human metapneumovirus 00-1  
 37 <400> SEQUENCE: 1  
 39 Met Ser Leu Gln Gly Ile His Leu Ser Asp Leu Ser Tyr Lys His Ala  
 40 1 5 10 15  
 43 Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr  
 44 20 25 30  
 47 Thr Ala Val Thr Pro Ser Ser Leu Gln Gln Glu Ile Thr Leu Leu Cys  
 48 35 40 45  
 51 Gly Glu Ile Leu Tyr Ala Lys His Ala Asp Tyr Lys Tyr Ala Ala Glu  
 52 50 55 60  
 55 Ile Gly Ile Gln Tyr Ile Ser Thr Ala Leu Gly Ser Glu Arg Val Gln  
 56 65 70 75 80  
 59 Gln Ile Leu Arg Asn Ser Gly Ser Glu Val Gln Val Val Leu Thr Arg  
 60 85 90 95  
 63 Thr Tyr Ser Leu Gly Lys Ile Lys Asn Asn Lys Gly Glu Asp Leu Gln  
 64 100 105 110  
 67 Met Leu Asp Ile His Gly Val Glu Lys Ser Trp Val Glu Glu Ile Asp  
 68 115 120 125  
 71 Lys Glu Ala Arg Lys Thr Met Ala Thr Leu Leu Lys Glu Ser Ser Gly  
 72 130 135 140  
 75 Asn Ile Pro Gln Asn Gln Arg Pro Ser Ala Pro Asp Thr Pro Ile Ile

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76	145	150	155	160												
79	Leu	Leu	Cys	Val	Gly	Ala	Leu	Ile	Phe	Thr	Lys	Leu	Ala	Ser	Thr	Ile
80																
83	Glu	Val	Gly	Leu	Glu	Thr	Thr	Val	Arg	Arg	Ala	Asn	Arg	Val	Leu	Ser
84																
87	Asp	Ala	Leu	Lys	Arg	Tyr	Pro	Arg	Met	Asp	Ile	Pro	Lys	Ile	Ala	Arg
88																
91	Ser	Phe	Tyr	Asp	Leu	Phe	Glu	Gln	Lys	Val	Tyr	His	Arg	Ser	Leu	Phe
92																
95	Ile	Glu	Tyr	Gly	Lys	Ala	Leu	Gly	Ser	Ser	Ser	Thr	Gly	Ser	Lys	Ala
96																
99	Glu	Ser	Leu	Phe	Val	Asn	Ile	Phe	Met	Gln	Ala	Tyr	Gly	Ala	Gln	
100																
103	Thr	Met	Leu	Arg	Trp	Gly	Val	Ile	Ala	Arg	Ser	Ser	Asn	Asn	Ile	Met
104																
107	Leu	Gly	His	Val	Ser	Val	Gln	Ala	Glu	Leu	Lys	Gln	Val	Thr	Glu	Val
108																
111	Tyr	Asp	Leu	Val	Arg	Glu	Met	Gly	Pro	Glu	Ser	Gly	Leu	Leu	His	Leu
112																
115	Arg	Gln	Ser	Pro	Lys	Ala	Gly	Leu	Leu	Ser	Leu	Ala	Asn	Cys	Pro	Asn
116																
119	Phe	Ala	Ser	Val	Val	Leu	Gly	Asn	Ala	Ser	Gly	Leu	Gly	Ile	Ile	Gly
120																
123	Met	Tyr	Arg	Gly	Arg	Val	Pro	Asn	Thr	Glu	Leu	Phe	Ser	Ala	Ala	Glu
124																
127	Ser	Tyr	Ala	Lys	Ser	Leu	Lys	Glu	Ser	Asn	Lys	Ile	Asn	Phe	Ser	Ser
128																
131	Leu	Gly	Leu	Thr	Asp	Glu	Glu	Lys	Glu	Ala	Ala	Glu	His	Phe	Leu	Asn
132																
135	Val	Ser	Asp	Asp	Ser	Gln	Asn	Asp	Tyr	Glu						
136																
139	<210>	SEQ	ID	NO:	2											
140	<211>	LENGTH:	391													
141	<212>	TYPE:	PRT													
142	<213>	ORGANISM:	Avian pneumovirus A													
144	<400>	SEQUENCE:	2													
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147	1					5				10						15
150	Ile	Leu	Glu	Asp	Ser	Gln	Tyr	Thr	Ile	Arg	Arg	Asp	Val	Gly	Ala	Thr
151									20		25					30
154	Thr	Ala	Ile	Thr	Pro	Ser	Glu	Leu	Gln	Pro	Gln	Val	Ser	Thr	Leu	Cys
155									35		40					45
158	Gly	Met	Val	Leu	Phe	Ala	Lys	His	Thr	Asp	Tyr	Glu	Pro	Ala	Ala	Glu
159									50		55					60
162	Val	Gly	Met	Gln	Tyr	Ile	Ser	Thr	Ala	Leu	Gly	Ala	Asp	Arg	Thr	Gln
163									65		70					80
166	Gln	Ile	Leu	Lys	Asn	Ser	Gly	Ser	Glu	Val	Gln	Gly	Val	Met	Thr	Lys
167									85		90					95
170	Ile	Val	Thr	Leu	Ser	Ala	Glu	Gly	Ser	Val	Arg	Lys	Arg	Glu	Val	Leu

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171 100 105 110  
 174 Asn Ile His Asp Val Gly Val Gly Trp Ala Asp Asp Val Glu Arg Thr  
 175 115 120 125  
 178 Thr Arg Glu Ala Met Gly Ala Met Val Arg Glu Lys Val Gln Leu Thr  
 179 130 135 140  
 182 Lys Asn Gln Lys Pro Ser Ala Leu Asp Ala Pro Val Ile Leu Leu Cys  
 183 145 150 155 160  
 186 Ile Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Val Glu Val Gly  
 187 165 170 175  
 190 Leu Glu Thr Ala Ile Arg Arg Ala Ser Arg Val Leu Ser Asp Ala Ile  
 191 180 185 190  
 194 Ser Arg Tyr Pro Arg Met Asp Ile Pro Arg Ile Ala Lys Ser Phe Phe  
 195 195 200 205  
 198 Glu Leu Phe Glu Lys Lys Val Tyr Tyr Arg Asn Leu Phe Ile Glu Tyr  
 199 210 215 220  
 202 Gly Lys Ala Leu Gly Ser Thr Ser Thr Gly Ser Arg Met Glu Ser Leu  
 203 225 230 235 240  
 206 Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln Thr Met Leu  
 207 245 250 255  
 210 Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Asn Ile Met Leu Gly His  
 211 260 265 270  
 214 Val Ser Val Gln Ala Glu Leu Arg Gln Val Ser Glu Val Tyr Asp Leu  
 215 275 280 285  
 218 Val Arg Lys Met Gly Pro Glu Ser Gly Leu Leu His Leu Arg Gln Ser  
 219 290 295 300  
 222 Pro Lys Ala Gly Leu Leu Ser Leu Thr Asn Cys Pro Asn Phe Ala Ser  
 223 305 310 315 320  
 226 Val Val Leu Gly Asn Ala Ala Gly Leu Gly Ile Ile Gly Met Tyr Lys  
 227 325 330 335  
 230 Gly Arg Ala Pro Asn Leu Glu Leu Phe Ala Ala Ala Glu Ser Tyr Ala  
 231 340 345 350  
 234 Arg Thr Leu Arg Glu Asn Asn Lys Ile Asn Leu Ala Ala Leu Gly Leu  
 235 355 360 365  
 238 Thr Asp Asp Glu Arg Glu Ala Ala Thr Ser Tyr Leu Gly Gly Asp Asp  
 239 370 375 380  
 242 Glu Arg Ser Ser Lys Phe Glu  
 243 385 390  
 246 <210> SEQ ID NO: 3  
 247 <211> LENGTH: 391  
 248 <212> TYPE: PRT  
 249 <213> ORGANISM: Avian pneumovirus B  
 251 <400> SEQUENCE: 3  
 253 Met Ser Leu Glu Ser Ile Arg Leu Ser Asp Leu Glu Tyr Lys His Ala  
 254 1 5 10 15  
 257 Ile Leu Asp Glu Ser Gln Tyr Thr Ile Arg Arg Asp Val Gly Ala Thr  
 258 20 25 30  
 261 Thr Ala Ile Thr Pro Ser Glu Leu Gln Pro Lys Val Ser Thr Leu Cys  
 262 35 40 45  
 265 Gly Met Ile Leu Phe Ala Lys His Ala Asp Tyr Glu Pro Ala Ala Gln

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266	50	55	60													
269	Val	Gly	Met	Gln	Tyr	Ile	Ser	Thr	Ala	Leu	Gly	Ala	Asp	Lys	Thr	Gln
270	65															80
273	Gln	Ile	Leu	Lys	Ser	Ser	Gly	Ser	Glu	Val	Gln	Gly	Val	Met	Thr	Lys
274																95
277	Ile	Val	Thr	Leu	Pro	Ala	Glu	Gly	Pro	Ile	Arg	Lys	Arg	Glu	Val	Leu
278																110
281	Asn	Ile	His	Asp	Ile	Gly	Pro	Ala	Trp	Ala	Asp	Asn	Val	Glu	Arg	Thr
282																125
285	Ala	Arg	Glu	Thr	Met	Ser	Leu	Met	Val	Lys	Glu	Lys	Ala	Gln	Ile	Pro
286																140
289	Lys	Asn	Gln	Lys	Pro	Ser	Ala	Leu	Asp	Ala	Pro	Val	Ile	Leu	Leu	Cys
290	145															160
293	Ile	Gly	Ala	Leu	Ile	Phe	Thr	Lys	Leu	Ala	Ser	Thr	Val	Glu	Val	Gly
294																175
297	Leu	Glu	Thr	Ala	Ile	Arg	Arg	Ala	Ser	Arg	Val	Leu	Ser	Asp	Ala	Ile
298																190
301	Ser	Arg	Tyr	Pro	Arg	Met	Asp	Ile	Pro	Arg	Ile	Ala	Lys	Ser	Phe	Phe
302																205
305	Glu	Leu	Phe	Glu	Lys	Lys	Val	Tyr	Tyr	Arg	Asn	Leu	Phe	Ile	Glu	Tyr
306	210															220
309	Gly	Lys	Ala	Leu	Gly	Ser	Thr	Ser	Ser	Gly	Ser	Arg	Met	Glu	Ser	Leu
310	225															240
313	Phe	Val	Asn	Ile	Phe	Met	Gln	Ala	Tyr	Gly	Ala	Gly	Gln	Thr	Met	Leu
314																255
317	Arg	Arg	Gly	Val	Val	Ala	Arg	Ser	Ser	Asn	Asn	Ile	Met	Leu	Gly	His
318																270
321	Val	Ser	Val	Gln	Ala	Glu	Leu	Arg	Gln	Val	Ser	Glu	Val	Tyr	Asp	Leu
322																285
325	Val	Arg	Lys	Met	Gly	Pro	Glu	Ser	Gly	Leu	Leu	His	Leu	Arg	Gln	Ser
326	290															300
329	Pro	Lys	Ala	Gly	Leu	Leu	Ser	Leu	Thr	Ser	Cys	Pro	Asn	Phe	Ala	Ser
330	305															320
333	Val	Val	Leu	Gly	Asn	Ala	Ala	Gly	Leu	Gly	Ile	Ile	Gly	Met	Tyr	Lys
334																335
337	Gly	Arg	Ala	Pro	Asn	Leu	Glu	Leu	Phe	Ser	Ala	Ala	Glu	Ser	Tyr	Ala
338																350
341	Arg	Ser	Leu	Lys	Glu	Ser	Asn	Lys	Ile	Asn	Leu	Ala	Ala	Leu	Gly	Leu
342																365
345	Thr	Glu	Asp	Glu	Arg	Glu	Ala	Ala	Thr	Ser	Tyr	Leu	Gly	Gly	Asp	Glu
346																380
349	Asp	Lys	Ser	Gln	Lys	Phe	Glu									
350	385															390
353	<210>	SEQ	ID	NO:	4											
354	<211>	LENGTH:	394													
355	<212>	TYPE:	PRT													
356	<213>	ORGANISM:	Avian pneumovirus C													
358	<400>	SEQUENCE:	4													
360	Met	Ser	Leu	Gln	Gly	Ile	Gln	Leu	Ser	Asp	Leu	Ser	Tyr	Lys	His	Ala

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361	1	5	10	15												
364	Ile	Leu	Lys	Glu	Ser	Gln	Tyr	Thr	Ile	Lys	Arg	Asp	Val	Gly	Thr	Thr
365																
		20					25								30	
368	Thr	Ala	Val	Thr	Pro	Ser	Ser	Leu	Gln	Arg	Glu	Val	Ser	Leu	Leu	Cys
369																
		35					40								45	
372	Gly	Glu	Ile	Leu	Tyr	Ala	Lys	His	Thr	Asp	Tyr	Ser	His	Ala	Ala	Glu
373																
		50					55								60	
376	Val	Gly	Met	Gln	Tyr	Val	Ser	Thr	Thr	Leu	Gly	Ala	Glu	Arg	Thr	Gln
377																
		65					70				75				80	
380	Gln	Ile	Leu	Lys	Asn	Ser	Gly	Ser	Glu	Val	Gln	Ala	Val	Leu	Thr	Lys
381																
		85					90				95					
384	Thr	Tyr	Ser	Leu	Gly	Lys	Gly	Lys	Asn	Ser	Lys	Gly	Glu	Glu	Leu	Gln
385																
		100					105				110					
388	Met	Leu	Asp	Ile	His	Gly	Val	Glu	Arg	Ser	Trp	Ile	Glu	Glu	Val	Asp
389																
		115					120				125					
392	Lys	Glu	Ala	Arg	Lys	Thr	Met	Ala	Ser	Ala	Thr	Lys	Asp	Asn	Ser	Gly
393																
		130					135				140					
396	Pro	Ile	Pro	Gln	Asn	Gln	Arg	Pro	Ser	Ser	Pro	Asp	Ala	Pro	Ile	Ile
397																
		145					150				155				160	
400	Leu	Leu	Cys	Ile	Gly	Ala	Leu	Ile	Phe	Thr	Lys	Leu	Ala	Ser	Thr	Ile
401																
		165					170				175					
404	Glu	Val	Gly	Leu	Glu	Thr	Ala	Val	Arg	Arg	Ala	Asn	Arg	Val	Leu	Asn
405																
		180					185				190					
408	Asp	Ala	Leu	Lys	Arg	Phe	Pro	Arg	Ile	Asp	Ile	Pro	Lys	Ile	Ala	Arg
409																
		195					200				205					
412	Ser	Phe	Tyr	Asp	Leu	Phe	Glu	Gln	Lys	Val	Tyr	Tyr	Arg	Ser	Leu	Phe
413																
		210					215				220					
416	Ile	Glu	Tyr	Gly	Lys	Ala	Leu	Gly	Ser	Ser	Ser	Thr	Gly	Ser	Lys	Ala
417																
		225					230				235				240	
420	Glu	Ser	Leu	Phe	Val	Asn	Ile	Phe	Met	Gln	Ala	Tyr	Gly	Ala	Gly	Gln
421																
		245					250				255					
424	Thr	Met	Leu	Arg	Trp	Gly	Val	Ile	Ala	Arg	Ser	Ser	Asn	Asn	Ile	Met
425																
		260					265				270					
428	Leu	Gly	His	Val	Ser	Val	Gln	Ala	Glu	Leu	Lys	Gln	Val	Thr	Glu	Val
429																
		275					280				285					
432	Tyr	Asp	Leu	Val	Arg	Glu	Met	Gly	Pro	Glu	Ser	Gly	Leu	Leu	His	Leu
433																
		290					295				300					
436	Arg	Gln	Asn	Pro	Lys	Ala	Gly	Leu	Leu	Ser	Leu	Ala	Asn	Cys	Pro	Asn
437																
		305					310				315				320	
440	Phe	Ala	Ser	Val	Val	Leu	Gly	Asn	Ala	Ser	Gly	Leu	Gly	Ile	Leu	Gly
441																
		325					330				335					
444	Met	Tyr	Arg	Gly	Arg	Val	Pro	Asn	Thr	Glu	Leu	Phe	Ala	Ala	Glu	
445																
		340					345				350					
448	Ser	Tyr	Ala	Arg	Ser	Leu	Lys	Glu	Ser	Asn	Lys	Ile	Asn	Phe	Ser	Ser
449																
		355					360				365					
452	Leu	Gly	Leu	Thr	Glu	Glu	Glu	Lys	Glu	Ala	Ala	Glu	Asn	Phe	Leu	Asn
453																
		370					375				380					
456	Ile	Asn	Glu	Glu	Gly	Gln	Asn	Asp	Tyr	Glu						
457																
		385					390									

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:105; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22  
Seq#:105; Xaa Pos. 29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47  
Seq#:105; Xaa Pos. 48  
Seq#:106; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22  
Seq#:106; Xaa Pos. 23,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47  
Seq#:106; Xaa Pos. 48  
Seq#:133; N Pos. 6  
Seq#:135; N Pos. 6,9  
Seq#:138; N Pos. 4  
Seq#:142; N Pos. 10,19  
Seq#:143; N Pos. 17

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:101,102,103,104,107,108,109,110,111,112,113,114,115,116,117,118,119,120  
Seq#:121,122,123,124,125,126,127,128,129,130,131,132,133,134,135,136,137,138  
Seq#:139,140,141,142,143,144,145,146,147,148,149,150,151,152,153,154,155,156  
Seq#:157,158,159,160,161,162,163,164,165

**VERIFICATION SUMMARY**  
**PATENT APPLICATION: US/10/722,045**

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L:6726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:105 after pos.:0  
M:341 Repeated in SeqNo=105  
L:6760 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106 after pos.:0  
M:341 Repeated in SeqNo=106  
L:7103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:133 after pos.:0  
L:7138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135 after pos.:0  
L:7180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:138 after pos.:0  
L:7239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:142 after pos.:0  
L:7257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:143 after pos.:0